2823021.5 601473661 BX448882

BX354591 602947063 AGENCOURT

AL557131

601589730

601334715 601513909

AL528496

601564420

. '<u>)</u>

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB e Maximum DB e

Database

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Distribution: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 719)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Unpublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Issue Procurement: ATCC/DCTD/DTP

6 CDNA Library Preparation: Ling Hong/Rubin Laboratory

6 CDNA Library Preparation: Ling Hong/Rubin Laboratory

7 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

8 Plate: LLCK136 row: h column: 10

8 High quality sequence stop: 777.
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adaptor: GGCAGCAG(G). Size-selected >S00bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                BE275002 719 bp mRNA linear EST 13-JUL-2000
601122536F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346617 5',
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BG751059 602729849
                     AL527192 F
B144196 E
B144296 E
B145296 E
AL518571 A
AL518571 A
B24734 S
B2744882 E
B2744882 E
B2744882 E
B2744892 E
B2744892 E
B273429 E
B273429 E
B273431772 E
B273439 E
B2533496 A
BE533496 E
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                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                 AL518571
AL518571
BEV24554
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AL557131
BI193429
CCF264787
BES331772
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Best Local Similarity
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                                                                                          February 11, 2005, 16:49:33; Search time 2179 Seconds (without alignments) 6079.103 Million cell updates/sec
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                                                                                                                                                                         1 TTCGAGGCGGGGGGGGC...........GGGCCATGTCCCCGATGTCA 348
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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                     34239544 Begs, 19032134700 residues
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                           US-09-824-134-1_COPY_388_735
348
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Maximum Match 100%
Listing first 45 summaries
                                                                    - nucleic search, using sw model
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Score

Result No.

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/lab.host="bull08 (phage resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE275052 774 bp mRNA linear EST 13-JUL-2000 601122604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346608 5',
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                                                                                                                      61 AACGICATAIGIGALAAIGIGGGAAAGAIIGGAGAAGGCIGGCICGICGAGCICAAAGIC 120
                                                                                                                                                                                                    TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCGCAACCTGACAGGCGTGTG 180
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                                        1 TTCGAGGCGGCGGCGGCCGGCCGCCTGGGGAAGAGAACTTGTGCAGCATTT 60
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(Mases 1 to 774)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM36 row: h column: 01
High quality sequence stop: 733.
Location/Qualifiers
                                                                                                                                                          196 AACGICATATGIGATAATGIGGGAAAGATIGGAGAAGGCIGGCICGICAGCICAAAGIC
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  0; Mismatches
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Homo sapiens
348; Conservative
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DB 2; Length 774;

100.0%; Score 348;

Query Match

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AGENCOURT 10622000 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6731271 5', mRNA-sequence.
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I (bases 1 to 850)
INH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                              257 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTCGAGGCGGGGGGGCCGCCGGGCCTGGGGAAGAGACTGTGTGCAGCATTT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can )
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3057 row: g column: 14
High quality sequence stop: 650.
Location/Qualifiers
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                           Indels
  Pred. No. 1.2e-83;
; Mismatches 0;
Local Similarity 100.0%; P:
nes 348; Conservative 0;
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/tissue type="goidermoid carcinoma, cell line"
/lab_hogt="DH10B (phage-resistant)"
/clone lib="NH1 MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhO1; Site_2: EcoR1; cDNA made by oligo-dT priming.
lib=celinomally cloned into EcoR1/KhO1 sites using the following 5' adaptor: gGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ672502
AGENCOURT_8349344 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6276350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-ramail.inh.gov
Email: capaba-ramail.inh.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2460 row: p column: 15
High quality sequence stop: 488.
Location/Qualifiers
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                                                                 Length 931;
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Note: this is a NIH_MGC Library."
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                                                             Query Match
100.0%; Score 348; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 348; Conservative 0; Mismatches 0;
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/clone="IMAGE:6276350"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 107"
/note="organ: breast, Vector: pOTB7; Site_1: ECORI;
Site_2: Xhol; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California. Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2740 row: h column: 01
High quality sequence stop: 506.
Location/Qualifiers
                                                                                                                                                                                                          TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG
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AGENCOURT 10217577 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6563185 5', mRNA sequence.
BU535532
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                              Length 850;
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                         Query Match
100.0%; Score 348; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 348; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ò 유 ð g ò d ò a ò 엄 ð 셤

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/tissue type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NNH MGC 102";
/note="Organ: allivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nh.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lnl.gov

Plate: LLCM2321 row: k column: 05

High quality sequence stop: 575.
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947 bp mRNA linear EST 04-SEP-2002
AGENCOURT_8045256 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6086524
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Pred. No. 1.3e-83;
0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6086524"
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BU197303
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FEATURES

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12. (Dases 1 to 965)

13. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

14. Pull-length cDNA libraries and normalization

15. Toun published (2001)

16. On Feb 15, 2001 this sequence version replaced gi:31270330.

17. Contact: Genoscope

18. Genoscope - Centre National de Sequencage

18. True Gaston Cremieux, CP 5706 - 91057 Testy Cedex - FRANCE

18. Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                constructed
following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synchesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Pred. No. 1.3e-83;
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Matches 348; Conservative 0
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1029 bp DNA linear GSS 15-DEC-2003
VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 1029)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1029)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Trodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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100.0%; Score 348; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 348; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Genoscope - Centre National de Sequencage
Z rue Gastono Cremieux, CP 5706 - 91057. EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL527771 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens AL527771 ACDNA COT 25-NORMALIZED Homo sapiens AL527771 AL527771
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/clone Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
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1 (bases 1 to 993)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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     /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ScoR vites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                             ; Score 348; DB 1;
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0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="CS0DC026YP18"
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1595 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CSODJ011YK23 of T cells (Jurkat cell line) CDt 10-normalized of Homo sapiens (human).
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Score 348;
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HTC; CNSLT_CDNA.
HOMO sapiens (human)
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1. (Dases 1 to 1134)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

3. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

4. Unpublished (2001)

5. Ton Gaboscope

6. Genoscope - Centre National de Sequencage

7. Tue Gaston Cremieux, CP 5706 - 91057 ERNY cedex - FRANCE

8. Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Scor V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/note="list strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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AL544558
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                                    Length 1029;
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                                       100.0%; Score 348; DB 9;
100.0%; Pred. No. 1.3e-83;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="CS0DI021Y021"
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                                       Query Match
Best Local Similarity 100.
Matches 348; Conservative
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Submission
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Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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Mammalia, Eutheria, Primates, Catarrhini, Hom
1. (bases 1 to 1595)
M. M. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Pred. No. 1.4e-83;
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328 TTCGAGGCGGGGGGGGGCGGGCCGCCTGGGGAAGAAGACCCTGTGTGCAGCATTT 387
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime into the Not I and CONA was digested with Not I and cloned into the Not I and Cloned was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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1595 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DK005YM20 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
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1 (bases 1 to 1595)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
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                                                                                                         TCAGACACCAAGATCGACATCGAGGACAGATACCCCGGCAACCTGACAGAGCGTGTG
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100.0%; Pred. No. 1.4e-83;
Live 0; Mismatches 0;
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Homo sapiens (human)
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
184 b: www.genoscope.cns.fr)
185 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Gaps
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/db_xref="texon:9606"
/clone="CSODI067YD16"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Mammalia, Butheria, Primates, Catarrhini, Hon
1 (bases 1 to 1614)
Li, W. Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
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HTC; CNSLT_CDNA.
Homo Bapiens (human)
Homo Bapiens
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 9100 GENYZ cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
191 9100 GENYZ cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
18t strand conscope.cns.fr)
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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        182 TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG
                                                                         602 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG
                                             181 CGGGAGTCACTGAGAATCTGGAAGAACACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG
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/tissue_type="T cells (Jurkat cell line)"
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100.0%; Pred. No. 1.4e-83;
ive 0; Mismatches 0;
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HTC; CNSLT cDNA.
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Homo sapiens
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Best Local Similarity 100.
Matches 348; Conservative
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Brill 9109106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized Library was constructed by Life Technologies, a division of Invitrogen.
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                                           TCAGACACCAAGATCGACAAGATCGAGGACAGATACCCCCGCAACCTGACAGAGCGTGTG 180
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                                                                     TTCGAGGCGGGGGGGCGGCCGGGCCGCGCTGGGGAAGAGCCTGTGTGCAGCATTT
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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25-normalized of Homo sapiens (human).
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                                                                                                                                                                                                                                                                                          301 CAGGCCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 348
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100.0%; Pred. No. 1.4e-83;
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Homo sapiens (human)
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